



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/042,894

Source: 01DE

Date Processed by STIC: 1/27/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**Raw Sequence Listing Error Summary**

**ERROR DETECTED**      **SUGGESTED CORRECTION**      **SERIAL NUMBER:** 10/042,894

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1  Wrapped Nucleic  
       Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
      Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6  PatentIn 2.0  
      "bug"      A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
      (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  Skipped Sequences  
      (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
      (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
      Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence.

11  Use of <220>  
      26-28      Sequence(s) 26-28 missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
      "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n  
      N      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

4 <110> APPLICANT: Shi, Jinrui  
5 Beach, Larry  
6 Wang, Hongyu  
7 Rafalski, Antoni J.  
8 Rebecca E. Cahoon  
10 <120> TITLE OF INVENTION: Novel Inositol Polyphosphate Kinase  
11 Genes and Uses Thereof  
13 <130> FILE REFERENCE: 1286  
15 <140> CURRENT APPLICATION NUMBER: US/10/042,894  
15 <141> CURRENT FILING DATE: 2002-01-09  
15 <150> PRIOR APPLICATION NUMBER: US 60/261,465  
16 <151> PRIOR FILING DATE: 2001-01-12  
18 <160> NUMBER OF SEQ ID NOS: 37  
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply  
Corrected Diskette Needed

*cross  
throughout*

## ERRORED SEQUENCES

104 <210> SEQ ID NO: 2  
105 <211> LENGTH: 240  
106 <212> TYPE: PRT  
107 <213> ORGANISM: Zea mays  
109 <400> SEQUENCE: 2  
110 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
111 1 5 10 15  
112 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
113 20 25 30  
114 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
115 35 40 45  
116 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
117 50 55 60  
118 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
119 65 70 75 80  
120 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Ala Gly  
121 85 90 95  
122 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
123 100 105 110  
124 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp  
125 115 120 125  
126 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser  
127 130 135 140  
128 Arg Arg Pro Arg Gly Arg Val Ala Asp Gly Ala Pro Gly Gly Glu  
129 145 150 155 160

R2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

130 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val  
131 165 170 175  
132 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys  
133 180 185 190  
134 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His  
135 195 200 205  
136 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe

E--> 137

210 215 220 <sup>↑ Trp Ala Met Met Leu Leu Gln Ser</sup>  
217 <210> SEQ ID NO: 4  
218 <211> LENGTH: 227  
219 <212> TYPE: PRT  
220 <213> ORGANISM: Zea mays  
222 <400> SEQUENCE: 4  
223 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
224 1 5 10 15  
225 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
226 20 25 30  
227 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
228 35 40 45  
229 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
230 50 55 60  
231 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
232 65 70 75 80  
233 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
234 85 90 95  
235 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
236 100 105 110  
237 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
238 115 120 125  
239 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
240 130 135 140  
241 Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
242 145 150 155 160  
243 Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
244 165 170 175  
245 Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly  
246 180 185 190  
247 Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly

E--> 248

195 200 205 <sup>↑ Val Val Arg Gly Ala Ala Ser Val</sup>  
338 <210> SEQ ID NO: 6  
339 <211> LENGTH: 289  
340 <212> TYPE: PRT  
341 <213> ORGANISM: Zea mays  
343 <400> SEQUENCE: 6  
344 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
345 1 5 10 15  
346 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
347 20 25 30  
348 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu Val Ala Phe Tyr

*insert hard return*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

349	35	40	45	
350	Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr			
351	50	55	60	
352	Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln			
353	65	70	75	80
354	Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly			
355	85	90	95	
356	Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp			
357	100	105	110	
358	Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp			
359	115	120	125	
360	Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg			
361	130	135	140	
362	Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val			
363	145	150	155	160
364	Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val			
365	165	170	175	
366	Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val			
367	180	185	190	
368	Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala			
369	195	200	205	
370	Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu			
371	210	215	220	
372	Leu Gly Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly			
373	225	230	235	240
374	Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly			
375	245	250	255	
376	Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe			
E-->	377			
	260	265	270	Val Ser Asp Ile Val Pro Glu Thr
474	<210> SEQ ID NO: 8			
475	<211> LENGTH: 289			
476	<212> TYPE: PRT			
477	<213> ORGANISM: Zea mays			
479	<400> SEQUENCE: 8			
480	Met Ser Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala			
481	1	5	10	15
482	Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr			
483	20	25	30	
484	Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr			
485	35	40	45	
486	Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr			
487	50	55	60	
488	Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln			
489	65	70	75	80
490	Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Ala Gly			
491	85	90	95	
492	Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp			
493	100	105	110	
494	Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp			

*Insert hard return*

RAW SEQUENCE LISTING  
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Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

495 115 120 125  
 496 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
 497 130 135 140  
 498 Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
 499 145 150 155 160  
 500 Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
 501 165 170 175  
 502 Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val  
 503 180 185 190  
 504 Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
 505 195 200 205  
 506 Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
 507 210 215 220  
 508 Leu Gly Tyr Asp Ala Ala Ala Val Ala Gly Gly Asp Gly Gly Gly  
 509 225 230 235 240  
 510 Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
 511 245 250 255  
 512 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
 E--> 513  
 260 265 270 Val Ser Asp Ile Val Pro Glu Thr  
 602 <210> SEQ ID NO: 10  
 603 <211> LENGTH: 279  
 604 <212> TYPE: PRT  
 605 <213> ORGANISM: Glycine max  
 607 <400> SEQUENCE: 10  
 608 Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp  
 609 1 5 10 15  
 610 Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro  
 611 20 25 30  
 612 Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser  
 613 35 40 45  
 614 Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser  
 615 50 55 60  
 616 Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly  
 617 65 70 75 80  
 618 Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr  
 619 85 90 95  
 620 Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His  
 621 100 105 110  
 622 Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg  
 623 115 120 125  
 624 Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp  
 625 130 135 140  
 626 Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser  
 627 145 150 155 160  
 628 Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn  
 629 165 170 175  
 630 Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val  
 631 180 185 190  
 632 Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu

hard return

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Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

633 195 200 205  
 634 Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr  
 635 210 215 220  
 636 Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu  
 637 225 230 235 240  
 638 Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn  
**E--> 639**  
 245 250 255 ↑ Phe Leu Gly Gly Leu Cys Ser Phe  
 739 <210> SEQ ID NO: 12  
 740 <211> LENGTH: 310  
 741 <212> TYPE: PRT  
 742 <213> ORGANISM: Eucalyptus grandis  
 744 <400> SEQUENCE: 12  
 745 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly  
 746 1 5 10 15  
 747 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 748 20 25 30  
 749 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser  
 750 35 40 45  
 751 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro  
 752 50 55 60  
 753 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro  
 754 65 70 75 80  
 755 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro  
 756 85 90 95  
 757 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala  
 758 100 105 110  
 759 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr  
 760 115 120 125  
 761 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn  
 762 130 135 140  
 763 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe  
 764 145 150 155 160  
 765 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn  
 766 165 170 175  
 767 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys  
 768 180 185 190  
 769 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys  
 770 195 200 205  
 771 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu  
 772 210 215 220  
 773 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro  
 774 225 230 235 240  
 775 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val  
 776 245 250 255  
 777 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile  
 778 260 265 270  
 779 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn  
**E--> 780**  
 275 280 285 ↑ Leu Gly Leu Lys Glu Asn Gly Phe  
 871 <210> SEQ ID NO: 14  
 hard return

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

872 <211> LENGTH: 295  
 873 <212> TYPE: PRT  
 874 <213> ORGANISM: Parthenium argentatum  
 876 <400> SEQUENCE: 14  
 877 Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu  
 878 1 5 10 15  
 879 Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 880 20 25 30  
 881 Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser  
 882 35 40 45  
 883 Phe Ser Ser Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro  
 884 50 55 60  
 885 Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His  
 886 65 70 75 80  
 887 Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser  
 888 85 90 95  
 889 Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser  
 890 100 105 110  
 891 Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser  
 892 115 120 125  
 893 Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp  
 894 130 135 140  
 895 Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly  
 896 145 150 155 160  
 897 Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro  
 898 165 170 175  
 899 Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu  
 900 180 185 190  
 901 Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met  
 902 195 200 205  
 903 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala  
 904 210 215 220  
 905 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala  
 906 225 230 235 240  
 907 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp  
 908 245 250 255  
 909 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu  
 910  
 E--> 260 265 270 ↑ Ile Lys Phe Ile Ser Asp Ile Leu  
 964 <210> SEQ ID NO: 16  
 965 <211> LENGTH: 111  
 966 <212> TYPE: PRT  
 967 <213> ORGANISM: Zea mays  
 969 <400> SEQUENCE: 16  
 970 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
 971 1 5 10 15  
 972 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
 973 20 25 30  
 974 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 975 35 40 45  
 hard return

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DATE: 01/27/2002

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

976 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
 977 50 55 60  
 978 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 979 65 70 75 80

E--&gt; 980

Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly ↑ 85

982 &lt;210&gt; SEQ ID NO: 17

983 &lt;211&gt; LENGTH: 643

984 &lt;212&gt; TYPE: DNA

985 &lt;213&gt; ORGANISM: Zea mays

987 &lt;220&gt; FEATURE:

988 &lt;221&gt; NAME/KEY: misc\_feature

989 &lt;222&gt; LOCATION: (1)...(643)

990 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

992 &lt;400&gt; SEQUENCE: 17

hard return

W--> 993 ggccgtccct gntttgtta accacccgc cccaaaatct ctttctccgc tgcgctgcaa 60  
 994 acccaccgtt tccaccatcg ccactcgta ccccttgcgc ccatagtccc cataccatgc 120  
 995 ccgacctcca cccggccggag caccaagtgc cgggtcaccg cccctccggc agcaagctgg 180  
 996 gcccgtcat cgacggctcc ggcctttct acaagccgct ccaggccggc gaccgtgggg 240  
 W--> 997 agcacgaggt cgccttctat gaggcggttct cgcgcacgc cgnctcccg gccccatcc 300  
 998 gagacacctt cttccccggg ttccacggca cgcgactct ccccacccgag ggcgcagccg 360  
 999 gggagccgca tccgcacctc gtcctcgacg acctctcgcc ggggttttag ggcgcctcg 420  
 1000 tcgcagacat caagatcgcc gccatcacgt ggccacccgag ttccggcggag ccctacatcg 480

E--&gt; 1001

ncaagtacct ngccaaggac cgccggacca cgagcggttct gctcggttcc cgcgctttgc 540gtccgagtcg tcggcccccga

1003 &lt;210&gt; SEQ ID NO: 18

1004 &lt;211&gt; LENGTH: 519

1005 &lt;212&gt; TYPE: DNA

1006 &lt;213&gt; ORGANISM: Zea mays

1008 &lt;220&gt; FEATURE:

1009 &lt;221&gt; NAME/KEY: misc\_feature

1010 &lt;222&gt; LOCATION: (1)...(519)

1011 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

1013 &lt;400&gt; SEQUENCE: 18

hard return

W--> 1014 ggtacggang aaaangtggaa gtcttgcac agtcgcgcga gctcaangcg tggttcgagg 60  
 1015 ggcagactct gttccacttc tactcggcgt cgattttct gggctatgtat gctgtgcag 120  
 W--> 1016 tcgcagcagg cggangtggg ggtggggtaa cagtaagct ggtggacttt gcccattgtgg 180  
 W--> 1017 cccgggttga tgggggtatt gaccacaact tcctggccgg gctctgtctt ctgatcaagt 240  
 1018 ttgtttctga cattgttcca gagactcctc agacgcagcc tttgggtctt tcttaagaaa 300  
 W--> 1019 agatcctggc attttcgatt tgataacaaa ggaancactt tcagctgcca aaaaaaaanc 360

E--&gt; 1020

accagtgaag atgaaaataa cattatttag gaaagttccg atnataaccc accanattta 420aaaaaaaaag gtcccaaatt

1022 &lt;210&gt; SEQ ID NO: 19

1023 &lt;211&gt; LENGTH: 353

1024 &lt;212&gt; TYPE: DNA

1025 &lt;213&gt; ORGANISM: Zea mays

1027 &lt;220&gt; FEATURE:

1028 &lt;221&gt; NAME/KEY: misc\_feature

1029 &lt;222&gt; LOCATION: (1)...(353)

1030 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

1032 &lt;400&gt; SEQUENCE: 19

1033 ctcaaggcat gtttggagga gcagactctg ttccacttct actcggcgat gattttctg

60

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

W--> 1034 ggctatgatg ctgctgcagt cgccancaggc ggaggtgggg gtggggtaac agtgaagctg 120  
1035 gtggacttgc cccatgtggc cgagggtgat ggggttgatt tgaccacaac ttcctggcgc 180  
E--> 1036  
agctctgcta gctgatcaag ttccgtttct tgacattgtt ccaganactc cttagacgcc 240agcctttggg tccttcctta  
1132 <210> SEQ ID NO: 21  
1133 <211> LENGTH: 111  
1134 <212> TYPE: PRT  
1135 <213> ORGANISM: Zea mays  
1137 <400> SEQUENCE: 21  
1138 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
1139 1 5 10 15  
1140 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr  
1141 20 25 30  
1142 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
1143 35 40 45  
1144 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
1145 50 55 60  
1146 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
1147 65 70 75 80  
E--> 1148  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly ↑ 85  
1256 <210> SEQ ID NO: 23  
1257 <211> LENGTH: 322  
1258 <212> TYPE: PRT  
1259 <213> ORGANISM: Parthenium argentatum  
1261 <400> SEQUENCE: 23  
1262 Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys  
1263 1 5 10 15  
1264 Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg  
1265 20 25 30  
1266 Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg  
1267 35 40 45  
1268 Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu  
1269 50 55 60  
1270 Ala Asp Glu Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr  
1271 65 70 75 80  
1272 Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn  
1273 85 90 95  
1274 Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp  
1275 100 105 110  
1276 Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp  
1277 115 120 125  
1278 Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu  
1279 130 135 140  
1280 Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr  
1281 145 150 155 160  
1282 Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly  
1283 165 170 175  
1284 Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser  
1285 180 185 190  
1286 Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser

RAW SEQUENCE LISTING  
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TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

1287 195 200 205  
1288 Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu  
1289 210 215 220  
1290 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp  
1291 225 230 235 240  
1292 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile  
1293 245 250 255  
1294 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln  
1295 260 265 270  
1296 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly  
1297 275 280 285  
1298 Glu Gly Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val

E--> 1299

290 295 300 ↑ Gly Ala Gly Trp Met Asp Asp Ala  
1414 <210> SEQ ID NO: 25  
1415 <211> LENGTH: 316  
1416 <212> TYPE: PRT  
1417 <213> ORGANISM: Zea mays  
1419 <400> SEQUENCE: 25  
1420 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe  
1421 1 5 10 15  
1422 Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His  
1423 20 25 30  
1424 Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys  
1425 35 40 45  
1426 Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val  
1427 50 55 60  
1428 Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp  
1429 65 70 75 80  
1430 Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser  
1431 85 90 95  
1432 Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu  
1433 100 105 110  
1434 Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr  
1435 115 120 125  
1436 Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His  
1437 130 135 140  
1438 Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr  
1439 145 150 155 160  
1440 Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys  
1441 165 170 175  
1442 Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp  
1443 180 185 190  
1444 Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val  
1445 195 200 205  
1446 Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val  
1447 210 215 220  
1448 Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu  
1449 225 230 235 240  
1450 Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala

hard return

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

1451 245 250 255  
1452 Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu  
1453 260 265 270  
1454 Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn  
1455 275 280 285

E--> 1456

Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val ↑ 290 295  
1494 <210> SEQ ID NO: 29  
1495 <211> LENGTH: 21  
1496 <212> TYPE: PRT  
1497 <213> ORGANISM: Artificial Sequence  
1499 <220> FEATURE:  
1500 <223> OTHER INFORMATION: consensus sequence  
1502 <400> SEQUENCE: 29

E--> 1503

Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu ↑ 1 5  
1505 <210> SEQ ID NO: 30  
1506 <211> LENGTH: 33  
1507 <212> TYPE: PRT  
1508 <213> ORGANISM: Artificial Sequence  
1510 <220> FEATURE:  
1511 <223> OTHER INFORMATION: consensus sequence  
1513 <221> NAME/KEY: VARIANT  
1514 <222> LOCATION: (1)...(33)  
1515 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1517 <400> SEQUENCE: 30

W--> 1518 Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

E--> 1519

1 5 10 15 ↑ Lys Xaa Gly Pro Leu Val Asp Asp  
1521 <210> SEQ ID NO: 31  
1522 <211> LENGTH: 33  
1523 <212> TYPE: PRT  
1524 <213> ORGANISM: Artificial Sequence  
1526 <220> FEATURE:  
1527 <223> OTHER INFORMATION: consensus sequence  
1529 <221> NAME/KEY: VARIANT  
1530 <222> LOCATION: (1)...(33)  
1531 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1533 <400> SEQUENCE: 31

W--> 1534 Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

E--> 1535

1 5 10 15 ↑ Lys Xaa Gly Pro Leu Ile Asp Asp  
1537 <210> SEQ ID NO: 32  
1538 <211> LENGTH: 33  
1539 <212> TYPE: PRT  
1540 <213> ORGANISM: Artificial Sequence  
1542 <220> FEATURE:  
1543 <223> OTHER INFORMATION: consensus sequence  
1545 <221> NAME/KEY: VARIANT  
1546 <222> LOCATION: (1)...(33)  
1547 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1549 <400> SEQUENCE: 32

W--> 1550 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

RAW SEQUENCE LISTING  
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TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

E--> 1551

1	5	10	15	↑ Lys Xaa Gly Pro Leu Val Asp Asp
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1553 <210> SEQ ID NO: 33  
1554 <211> LENGTH: 33  
1555 <212> TYPE: PRT  
1556 <213> ORGANISM: Artificial Sequence  
1558 <220> FEATURE:  
1559 <223> OTHER INFORMATION: consensus sequence  
1561 <221> NAME/KEY: VARIANT  
1562 <222> LOCATION: (1)...(33)  
1563 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1565 <400> SEQUENCE: 33

Same error

W--> 1566 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

E--> 1567

1	5	10	15	↑ Lys Xaa Gly Pro Leu Ile Asp Asp
---	---	----	----	-----------------------------------

1569 <210> SEQ ID NO: 34  
1570 <211> LENGTH: 41  
1571 <212> TYPE: PRT  
1572 <213> ORGANISM: Artificial Sequence  
1574 <220> FEATURE:  
1575 <223> OTHER INFORMATION: consensus sequence  
1577 <221> NAME/KEY: VARIANT  
1578 <222> LOCATION: (1)...(41)  
1579 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1581 <400> SEQUENCE: 34

Same

W--> 1582 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp

1583	1	5	10	15
------	---	---	----	----

E--> 1584

Val	Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr	↑	20
-----	---	---	----

1586 <210> SEQ ID NO: 35  
1587 <211> LENGTH: 41  
1588 <212> TYPE: PRT  
1589 <213> ORGANISM: Artificial Sequence  
1591 <220> FEATURE:  
1592 <223> OTHER INFORMATION: consensus sequence  
1594 <221> NAME/KEY: VARIANT  
1595 <222> LOCATION: (1)...(41)  
1596 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1598 <400> SEQUENCE: 35

Same

W--> 1599 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp

1600	1	5	10	15
------	---	---	----	----

E--> 1601

Ile	Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr	↑	20
-----	---	---	----

1603 <210> SEQ ID NO: 36  
1604 <211> LENGTH: 41  
1605 <212> TYPE: PRT  
1606 <213> ORGANISM: Artificial Sequence  
1608 <220> FEATURE:  
1609 <223> OTHER INFORMATION: consensus sequence  
1611 <221> NAME/KEY: VARIANT  
1612 <222> LOCATION: (1)...(41)  
1613 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
1615 <400> SEQUENCE: 36

Same

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

W--> 1616 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
1617 1 5 10 15  
E--> 1618  
Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Glu Xaa Tyr <sup>T</sup> 20  
Same

*See next page for more entries*

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<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

see item 11 on Exam Summary Sheet

<220>

<221> primer bind

<222> (1)...(25)

<223> ~~for this numeric identifier and response are mandatory whenever~~ (213)

response is

<400> 26

accgcttcca ccatcgccac tcgtc

25 Unknown

or

Artificial Sequence

same error in seqs. 27-28

pwk

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:48

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:137 M:252 E: No. of Seq. differs, <211>LENGTH:Input:240 Found:224 SEQ:2  
L:248 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:4  
L:248 M:252 E: No. of Seq. differs, <211>LENGTH:Input:227 Found:208 SEQ:4  
L:377 M:252 E: No. of Seq. differs, <211>LENGTH:Input:289 Found:272 SEQ:6  
L:513 M:252 E: No. of Seq. differs, <211>LENGTH:Input:289 Found:272 SEQ:8  
L:639 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:10  
L:639 M:252 E: No. of Seq. differs, <211>LENGTH:Input:279 Found:256 SEQ:10  
L:780 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:12  
L:780 M:252 E: No. of Seq. differs, <211>LENGTH:Input:310 Found:288 SEQ:12  
L:910 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:14  
L:910 M:252 E: No. of Seq. differs, <211>LENGTH:Input:295 Found:272 SEQ:14  
L:980 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:16  
L:980 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:1001 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:17  
L:993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1001 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1001 M:252 E: No. of Seq. differs, <211>LENGTH:Input:643 Found:480 SEQ:17  
L:1020 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:18  
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1020 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1020 M:252 E: No. of Seq. differs, <211>LENGTH:Input:519 Found:360 SEQ:18  
L:1036 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:19  
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1036 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1036 M:252 E: No. of Seq. differs, <211>LENGTH:Input:353 Found:180 SEQ:19  
L:1148 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:21  
L:1148 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:1248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22  
L:1299 M:252 E: No. of Seq. differs, <211>LENGTH:Input:322 Found:304 SEQ:23  
L:1456 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:25  
L:1456 M:252 E: No. of Seq. differs, <211>LENGTH:Input:316 Found:288 SEQ:25  
L:1467 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1479 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1491 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1503 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:29  
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1519 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:30  
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1535 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:31  
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:1551 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:32  
L:1566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:48

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

L:1567 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:33  
L:1582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1584 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:34  
L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1601 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:35  
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:1618 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:36  
L:1633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1635 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:37